

Figure 1.

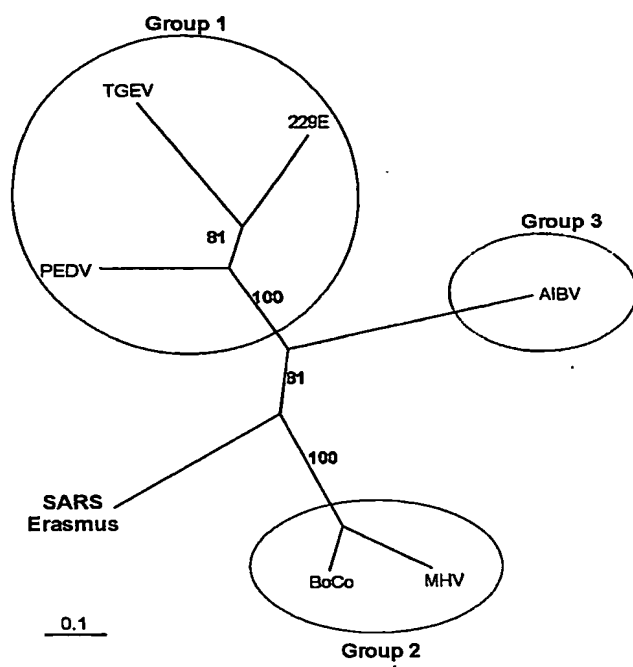


Figure 2 RNA sequences, implied polypeptides and alignment with one close relative

EMC-1

5 UUGUAAACUGGUGGUCUUGUACAACAGACUUCUCAGUGGUUGUCUAAUCUUUUGGGCACUACUGGUUGAAAAAC
 UCAGGCCUAUCUUUGAAUGGAUUGAGGCGAAACUUAGUGCAGGAGUUGAAUUUCUCAAGGAUGCUUGGGAGAU
 UCUCAAAUUUCUCAUUACAGGUGUUUUUGACAUCGUCUACAGGGUCAAAUACAGGUUGCUUCAGAUAAACAUCAAG
 GAUUGUGUAAAUGCUUCAUUGAUGUUGUUAACAAGGCACUCGAAUUGUGCAUUGAUCAAGUCACUAUCGCUG
 GCGCAAAGUUGCGAUCACUACAACUAGGUGAAGUCUUCACGCUCAAAGCAAGGGACUUUACCGUCAGUGUAU
 10 ACGUGGCAAGGAGCAGCUGCAACUACUCAUGCCUCUCUUAAGGCACCAAAGAAGUAACCUUUCU
 UGAAGGUGAUUCACAUGACACAGUACUUAACCUCUGAGGAGGUUGUUCUCAAGAACGGUGAA
 CUCGAAGCACUCGAGACGCCCUGUAGAUAGCUUCACAAAUGGAGCUAUCGUUGGCACACCAG
 UCUGUGUAAAUGGCCUCAUGCUCUUAAGAGAUUAAGGACAAAGAACAUAUCUGCGCAUUGUC
 UCCUGGUUUACUGGCUACAAACAAUGUCUUAUCGCUUAAAAGGGGGUGCACCAAUUAAGGU
 15 GUAACCUUUGGAGAAGAUACUGUUUGGGAAGUUCAGGGUUAACAAGAAUGUGAGAAUCACAU
 UUGAGCUUGAUGAACGUGUUGACAAAGUGCUUAAUGAAAAGUGCUCUGUCUACACUGUUGA
 AUCCGGUACCGAAGUACUGAGUUUGCAUGUGUUGUAGCAGAGGCUGUUGUGAAGACUUUA
 CAACCAGUUUCUGAUC

20 **Translation** Nucleotides 7 to 870: Frame 1; 288 aa

LVLVLYNRLLSGCLIFWALLVEKLRPIFEWIEAKLSAGVEFLKDAWEILKFLITGVFDIVKGQIQVASDNIKDCVKCFIDVV
 NKALEMCIDQVTIAGAKLRSLNLGEVFIAQSKGLYRQCIRGKEQLQLLMPKAPKEVTFLEGDSHDTVLTSEEVVLKNGEL
 EALETVPDSFTNGAIVGTPVCVNLMLLEIKDKEQYCALSPGLLATNNVFRKGGAPIKGVTFGEDTVWEVQGYKNVRITF
 ELDERVDKVLNEKCSVYTVESGTEVTEFACVVAEAVVKTLQPVSD

25 **Alignment**

RNA-directed RNA polymerase (orfla) murine hepatitis virus
 Identities = 72/285 (25%), Positives = 118/285 (41%)

30 Query: 49 FWALLVEKLRPIFEWIEAKLSAGVEFLKDAWEILKFLITGVFDIVKGQIQVASDNIKDCV 228
 F AL V +R I EW + L+ + W + L+ G+F + G I + + + V
 Sbjct: 638 FKALGVAVVRKITEWFD--LAVDIAASAAGWLCYQ-LVNGLFAVANGVITFVQE-VPELV 693

35 Query: 229 KCFIDVVNKALEMCIDQVTIA---GAKLRSLNLGEVFIAQSKGLYRQCIRGKEQLQLLMP 399
 K F+D ++ ID ++++ G + V +A SK +Y + K +MP
 Sbjct: 694 KNFVDKFKAFFKVLIDSMVSILSGLTVVKTASNRVCLAGSK-VYE--VVQKSLSAYVMP 750

40 Query: 400 LKAPKEVTFLEGDSHDTVLTSEEVVLKNGEL--EALETVPDSFTNGAIVGTPVCVNLML 573
 + E T L G+ V + V + L + P SF IV L
 Sbjct: 751 VGC-SEATCLVGEIEPAVFEDDVVDVVKAPLTYQGCKPPTSFEKICIVDK-----L 801

45 Query: 574 LEIKDKEQYCAL-----SPGLLATNNVFRKGGAPIKGVTFGEDT-VWEVQGYKNVRITF 735
 K +Q+ + + G+L F G K V F + V ++ + ++ITF
 Sbjct: 802 YMAKCGDQFYFVVVDNDTVGLDQCWRFPFCAG----KKVEFNDKPKVRKIPSTRKIKITF 857

50 Query: 736 ELDERVDKVLNEKCSVYTVESGTEVTEFACVVAEAVVKTLQPVSD 870
 LD D VL++ CS + V+ + E VV +AV TL P +
 Sbjct: 858 ALDATFDSVLSKACSEFEVDKDVTLDELDDVVLDAVESTLSPCKE 902

EMC-14

55 CAUCCAGCUUCUUAAGGCAGCAUAUGAAAAUUUCAAUUCACAGGACAUCUUACUUGCACCAUUGUUGUCAGCA
 GGCAUAUUUGGUGCUAAACCACUUCAGUCUUUACAAGUGUGCGUGCAGACGGUUCGUACACAGGUUUUAUUG
 CAGUCAUAGACAAAGCUCUUUAUGAGCAGGUUGUCAUGGAUUAUCUUGAUAAACCUGAAGCCUAGAGUGGAAGC
 ACCUAAACAAGAGGAGCCACCAAACACAGAAGAUUCCAAAACUGAGGAGAAAUCUGUCGUACAGAAGCCUGUC
 GAUGUGAAGCCAAAAAUUAAGGCCUGCAUUGAUGAGGUUACCACAACACUGGAAGAAACUAAGUUUCUUACCA
 AUAAGUUACUCUUGUUUGCUGAUUAUCAAUGGUAAGCUUUACCAUGAUUCUCAGAACAUAGCUUAGAGGUGAAGA
 UAUGUCUUUCCUUGAGAAGGAUGCACCUCUACAUGGUAGGUGAUGUUUAUCACUAGUGGUGAUUAUCACUUGUGUU

Fig. 2 Cont.

GUAAUACCCUCCAAAAAGGCUGGUGGCACUACUGAGAUGCUCUCAAGAGCUUUGAAGAAAGUGCCAGUUGAUG
AGUAUAUAACCACGUACCCUGGACAAGGAUGUGCUGGUUAUACACUUGAGGAAGCUAAGACUGCUCUUAAGAA
AUGCAAUUCUGCAUUUUUAUGUACUACCUUCAGAAGCACCUAUUGCUAAGGAAGAGAUUCUAGGAACUGUAUCC
UGGAAUUGAG

Translation

Nucleotides 5 to 739: Frame 2; 245 aa

IQLLKAAYENFNSQDILLAPLLSAGIFGAKPLQSLQVCVQTVRTQVYIAVNDKALYEQVMDYLDNLKPRVEAPKQEEPPN
TEDSKTEEKSVVQKPVVDVKPKIKACIDEVTTTLEETKFLTNKLLLFADINGKLYHDSQNMLRGEDMSFLEKDAPYMGVDVI
TSGDITCVVIPSKKAGGTTEMLSRALKKVPVDEYITTPGQGCAGYTLLEEAKTALKKCKSAFYVLPSEAPNAKEEILGTVS
WN

Alignment

replicase polyprotein lab Human coronavirus 229E

Identities = 48/202 (23%), Positives = 83/202 (41%), Gaps = 13/202 (6%)
Frame = +2

Query: 8 LLKAAYENFNSQDILLAPLLSAGIFGAKPLQSLQVCVQTVRT---QVYIAVNDKALYEQV 178
L+KA N Q L P+LS GIFG K SL+V + T +V++ + + +
Sbjct: 1371 LIKAYNTINNEQGTPLTPILSCGIFGIKLETSLEVLLDVCNTKEVKVFVYTDTEVCKVKD 1430
Query: 179 VMDYLDNLKPRVEAPKQEEPPNTEDSKTEEKSVVQKPVVDVKPKIKACIDEVTTTLEETKF 358
+ L N++ +VE PK E P V KP V K +++ ++
Sbjct: 1431 FVSGLVNVQ-KVEQPKIEPKP-----VSVIKVAPKPYRVDGKFSYFTEDLLCVADDKPI 1483
Query: 359 L--TNKLLLFADINGKLYHDSQNMLRG--EDMSFLEKDAP-----YMGVDVITSGDITC 508
+ T+ +L D L + +L +D + K P + +G V+ +
Sbjct: 1484 VLFTDSMLTLDDRGLALDNLASGVLSAAIKDCVDINKAIPSGNLIKFDIGSVV----VYM 1539
Query: 509 VVIPSKKAGGTTEMLSRALKKV 574
V+PS+K + R +K+
Sbjct: 1540 CVVPSEKDKHLDNNVQRCTRKL 1561

EMC-2

UCGAGAUUUcAUcUUGACGGUGCAGGUUCUUUCACUUGACAAACUAAAGAGUCUCUUAUCCCCUGCGGGAGGUU
AAGACUAUAAAAGUGUUCACAACUGUGGACAACACUAAUCUCCACACACAGCUUGUGGAUAUGUCUAUGACAU
AUGGACAGCAGUUUGGUCCAACAUACUUGGAUGGUGCUGAUGUUACAAAAUUAACCUCUAUGUAAAUCAUGA
GGGUAAGACUUUCUUUGUACUACCUAGUGAUGACACACUACGUAGUGAAGCUUUCGAGUACUACCAUACUCUU
GAUGAGAGUUUUUCUUGGUAGGUACAUGUCUGCUUUAACCACACAAAGAAAUGGAAA

Translation

Nucleotide 2 to 349: Frame 2; 116 aa

RDFILTVQVLSLDKLSLLSLREVKTIKVFTTVDNTNLHTQLVDMSMTYGQQFGPTYLDGADVTKIKPHVNHEGKTFVFLP
SDDTLRSEAFEYYHTLDESFLGRYMSALNHTKKWK

Alignment

> Bovine Coronavirus RNA-Dependent RNA polymerase

Identities = 25/90 (27%), Positives = 44/90 (48%)
Frame = +2

Query: 80 IKVFTTVDNTNLHTQLVDMSMTYGQQFGPTYLDGADVTKIKPHVNHEGKTFVFLPSDDTL 259
+ + TVD N + V + ++G+ G + DG +VTK K +N++GK FF + +
Sbjct: 1565 VDILLTVDGVNFTNRFVPVGESEFGKSLGNVFCGYNVTKHKCDINYGKGVFFQFDNLSSE 1624
Query: 260 RSEAFEYYHTLDESFLGRYMSALNHTKKWK 349
+A D+ L Y + L + KW+
Sbjct: 1625 DLKAVRSSFNFDQKELLAYYNMLVNCWKQ 1654

Fig. 2 Cont.

EMC13:

CUGAAGAAGUAGUGGaAAAUCCUACCAUACAGAAGGAAGUCAUAGAGUGUGACGUGAAAACUACCGAAGUUGU
 AGGCAAUGUCAUACUUAACCAUCAGAUGAAGGUGUUAAGUAACACAAGAGUUAGGUCUAGAGGAUCUUAUG
 GCUGCUUAUGUGGAAAACACAAGCAUUAACCAUUAAGAAACCUAUAGAGCUUUCACUAGCCUUAAGGUUUAAAAA
 5 CAAUUGCCACUCAUGGUUAUUGCUGCAAUUAAUAGUGUCCUUGGAGUAAAAUUUUGGCUUAUGUCAAAACCAU
 CUUAGGACAAGCAGCAAUUACAACAUCAAAUUGCGCUAAGAGAUUAGCACACGUGUGUUUAACAAUUAUAG
 CCUUAUGUGUUUACAUUAUUGUUCCAAUUGUGUACUUUUACUAAAAGUACCAUUCUAGAAUUAAGAGCUUCAC
 UACCUACAACUAUUGCUAAAAAUAGUGUUAAGAGUGUUGCUAAAAUUAUGUUUGGAUGCCGGCAUUAUUAUAGU
 10 GAAGUCACCCAAAUUUUCUAAAUUGUUCACAAUCGCUAUGUGGCUAUUGUUGUUAAGUAUUUGCUUAGGUUCU
 CUAAUCUGUGUAACUGCUGCUUUUGGUGUACUCUUAUCUAAUUUUGGUGCUCCUUCUUAUUGUAUUGGCGUUA
 GAGAAUUGUAUCUUAUUCGUCUACGUAACUACUAGGAUUUCUGUGAAGGUUCUUUUCCUUGCAGCAUUG
 UUUAAUGUGGAUUAAGACUCCCUUGAUUCUUAUCCAGCUCUUGAAACCAUUCAGGUGACGAUUUCAUCGUACAAG
 CUAGACUUGACAAUUUUAGGUCUGGCCGCGUG

Translation

>~out: 3 to 833: Frame 3 277 aa

EEVVENPTIQKEVIECDVKTTEVVGNVILKPSDEGVKVTQELGHEDLMAAYVENTSITIKKPNELSLALGLKTIATHGIAA
 INSVPSKILAYVKPFLGQAAITTSNCAKRLAQRVFNNYPYVFTLLFQLCTFTKSTNSRIRASLPTTIKNSVKSVAKLC
 20 LDAGINIVKSPKFSKLFITIAMWLLLLSICLSLICVTAAFGVLLSNFGAPSYCNGVRELYLNSSNVTMTDFCEGSFPCISIC
 LSGLDSDLSYPALETIQVTISSYKLDLTILGLAA

Alignment

bovine coronavirus RNA-dependent RNA Polymerase

Identities = 50/269 (18%),

25 Query: 57 KTTEVVGNVILKPSDEGVKVTQELGHEDLMAAYVENTSITIKKPNELSLALGLKTIATH- 233
 K +V +VI+ +K + L D+ ++ ++ N+LS+A+ + TI
 Sbjct: 2046 KPEKVEDSVIVNDDTSEIKYVKSLSIVDVYDMWLTGCRYVVRTANDLSMAVNVPTIRKFI 2105

30 Query: 234 --GIAAINSVPWSKI-LAYVKPFLGQAAITTSNCAKRLAQRVFN--NYMPYVFTLLF--- 389
 G+ + S+P + L +KP N K + ++ N++ ++F LLF
 Sbjct: 2106 KFGMTLV-SIPIDLLNLREIKPVF-----NVVKAVRNKISACFNFIKWLFVLLFGWI 2156

35 Query: 390 -----QLCTFTKSTNSRIRASLPTTIKNSVKSVAKLCLDAGINIVKSPKFSKLFITIAMW 554
 +T S++ L KN+ + + G + + +W
 Sbjct: 2157 KISADNKVIYTTTEVASKLTCKLVALAKNAFLTFFKWSVVARGACIIAT-----IFLLW 2209

Query: 555 XXXXXXXXXXXXXVTAAFGVLLSNFGAPSYCNGVRELYLNSSNVTM----- 695
 G L P++ + + ++ ++ T+
 40 Sbjct: 2210 FNFIYANVIFSDFYLEPKIGFL-----PTFVGKIAQWIKSTFSLVTICDLYSIQDVGFKN 2263

Query: 696 DFCEGSFPCISICLSGLDSDLSYPALETIQ 782
 +C GS C CL+G D LD+Y A++ +Q
 Sbjct: 2264 QYCNGSIACQFCLAGFMDLDNYKAIDVVQ 2292

EMC-3

GUGGUAAGAUUGUUAGUACUUGUUUUAACUUAUGCUUAAGGCCACAUAUUGUGCGUUCU
 UGCUGCAUUAUGUUUGUUAUUCGUUAUGCCAGUACAUAUUGUCAUCCAUGAUGGUUAC
 ACAAAUGAAAUCAUUGGUUACAAAGCCAUUCAGGAUGGUGUCACUCGUGACAUAUUCUA
 50 CUGAUGAUUGUUUGCAAUUAACAUGCUGGUUUUGACGCAUGGUUUAGCCAGCGUGGUGG
 UUCAUACAAAAUGACAAAAGCUGCCCUGUAGUAGCUGCUAUAUUAACAAGAGAGAUUGGU
 UUCAUAGUGCCUGGCUUACCGGGUACUGUGCUGAGAGCAAUCAAUGGUGACUUCUUGCAU
 UCCUACCUCGUGUUUUUAGUGCUGUUGGCAACAUAUUGCUACACACCUUCCAAACUCAUUGA
 GUAUAGUGAUUUUGCUACCUCU

Translation

Nucleotide 3-449; 149 aa

GKIVSTCFKMLKATLLCVLAALVCYIVMPVHTLSIHGYTNEIIGYKAIQDGVTRDIIISTDDCFANKHAGFD
 AWFSQRGGSYKNDKSCPVAAIITREIGFIVPGLPGTVLRAINGDFLHFLPRVFSAVGNICYTPSKLIEYSDF
 60 ATS

Fig. 2. Cont.

Alignment

> Murine Hepatitis Virus RNA-Dependent RNA polymerase

5 Identities = 48/126 (38%),

Query: 78 YIVMPVHTLSIHDGYTNEIIGYKAIQDGVTRDIISTDDCFANKHAGFDWFSQRRG--SY 251
 + +MP + + D +K I +GV RD+ TD CFANK FD W+ G Y
 Sbjct: 2859 WALMPTYAVHKSDMQLPLYASFVIDNGVLRDVSVDACFANKFNQFDQWYESTFGLAYY 2918

10 Query: 252 KNDKSCPVVAAIITREIGFIVPGLPGTVLRAINGDFLHFLPRVFSAVGNICYTPSKLIEY 431
 +N K+CPVV A+I ++IG + +P TVLR LHF+ F+ CYTP I Y
 Sbjct: 2919 RNSKACPVVVAVIDQDIGHTLNFVPTTVLR-YGFHVLHFITHAFATDSVQCYTPHMQIPY 2977

15 Query: 432 SDFATS 449
 +F S
 Sbjct: 2978 DNFYAS 2983

EMC-4

20 ACAGACAUAUACACUUCUGCUGUUCUGCAGAGUGGUUUUAGGAAAAUGGCAUUCGCGUCAGGCAAAGUUGAA
 GGGUGCAUGGUACAAGUAACUGUGGAACUACAACUCUUAUUGGAUUGUGGUUGGAUGACACAGUAUACUGUC
 CAAGACAUGUCAUUUGCACAGCAGAGACAUGCUUAAUCCUAACUAUGAAGAUUCUGCUCAUUCGCAAUCCAA
 CCAUAGCUUUUCUUGUUCAGGCUGGCAAGUUAACUUCGUGUUAUUGGCCAUUCUAUGCAAAAUUGUCUGCUU
 AGGCUUAAAGUUGAUACUUCUAACCCUAAGACACCCAAGUAUAAUUGUCCGUAUCCAACUGGCUAAACAU
 25 UUCAGAUUCUAGCAUGCUACAAGUGUUCACCAUCUGGUGUUAUACAGUGUGCCAUGAGACCUAUACAUACCAU
 UAAAGGUUCUUAUUGGAUCAUGUGGUAGUGUUGGUUUUAACAUAUGAUUAUGAUUGCGUGUCUUCUGC
 UAUUAGCAUCAUAUGGAGCUUCCAACAGGAGUACACGUGGUACUGACUUAAGAAGGUAAAUUCUAUGGUCCA
 UUGUUGACAGACAAACUGCACAGGUGCAGGUACAGACACAACCAUAACAUAUAAUGUUUUGGCAUGGCUGUA
 UGCUGCUGUUAUCAUGGUGUAU

Translation

Nucleotides 2 to 679: Frame 2; 226 aa

QTSITSAVLQSGFRKMAFSPGKVEGCMVQVTCGTTTLNGLWLDDEVYCPRHVICTAEDMLNPYEDLLIRKSNHSLVQAG
 NVQLRVIGHSMQNCLRLKVDTSNPKTPKYKVFRIQPGQTFSVLACYNGSPSGVYQCAMPNHTIKGSFLNGSCGSVGFNI
 35 DYDCVSFCYMHMELPTGVHAGTDLEGKFYGFVDRQTAQAAGTDTTITLNLVLAWLAAVINGD

Alignment

RNA-directed RNA polymerase murine hepatitis virus

40 Identities = 122/222 (54%)

Query: 8 SITSAVLQSGFRKMAFSPGKVEGCMVQVTCGTTTLNGLWLDDEVYCPRHVICTAEDMLNP 187
 S+T++ LQSG KM P+ KVE C+V VT G TLNGLWLD DEVYCPRHVIC++ DM +P
 45 Sbjct: 3326 SVTTSFLQSGIVKMSPTSKEPCIVSVTYGNMTLNLGLWLDDEVYCPRHVICSSADMTDP 3385

Query: 188 NYEDLLIRKSNHSLVQAGNVQLRVIGHSMQNCLRLKVDTSNPKTPKYKVFRIQPGQTF 367
 +Y +LL R ++ F V +G + L V+ + MQ C L L V NP TPKY F ++PG+TF
 50 Sbjct: 3386 DYPNLLCRVTSSDFCVMSGRMSLTVMYSQMGCQLVLTVTLQNPNTPKYSFGVVKPGETF 3445

Query: 368 SVLACYNGSPSGVYQCAMPNHTIKGSFLNGSCGSVGFNIDYDCVSFCYMHMELPTGVH 547
 +VLA YNG P G + +R +HTIKGSFL GSCGSVG+ + D V F YMH +EL TG H
 55 Sbjct: 3446 TVLAAYNRPQGAHVTLRSSHTIKGSFLCGSCGSVGVLGTGDSVRFVYMHQLELSTGCH 3505

Query: 548 AGTDLEGKFYGFVDRQTAQAAGTDTTITLNLVLAWLAAVIN 673
 GTD G FYGP+ D Q Q D T T+NV+AWLYAA+ N
 Sbjct: 3506 TGTDFSGNFYGPYRDAQVVLQVQDYTQTVNVVAVWLYAAIFN 3547

EMC-5

60 Note that this sequence is not fully in frame.

AGUUGGAAAAGAUGGCAGAUACAGGCUAUGACCCAAAUGUACAAACAGGCAAGAUCUGAGGA
 CAAGAGGGCAAAGUAACUAGUGCUAUGCAAACAAUGCUCUUCACUAUGCUUAGGAAGCUU
 GAUAAUGAUGCACUUAACAACAUUAUCAACAUGCGCGUGAUGGUUGUGUCCACUCAACA
 UCAUACCAUUGACUACAGCAGCCAAACUCAUGGUUGUUGUCCUGAUUAUGGUACCUACAA
 65 GAACACUUGUGAUGGUAACACCUUUAUCAUAUGCAUCUGCACUCUGGGAAAUCCAGCAAGUU
 GUUGAUGCGGAUAGCAAGAUUGUUAACUUAUGUGAAAUAACAUGGACAAUUCACCAAU
 UGGCUUGGCCCCUUAUUGUUAACAGCUCUAAGAGCCAAACUCAGCUGUUAACUACAGAAUAA
 UGAACUGAGUCCAGUAGCACUACGACAGAUGUCCUGUGCGGCUGGUACACACAAACAGCU
 UGUACUGAUGACAAUGCACUUGCCUACUUAACAUAUUCGAAGGGAGGUAGGUUUGUGCUGG

Fig. 2. Cont.

CAUUACUAUCAGACCACCAAGAUCUCAAAUGGGCUAGAUUCCCUAAGAGUGAUGGUACAGG
 UACAAUUUACACAGAACUGGAACCACCUUGUAGGUUUGUACAGACACACCAAAGGGCCU
 AAAGUGAAAUACUUGUACUUAUCAAGGCUUAAACAACCUAAAUAGAGGUUAGGUGCUGGG
 CAGUUUAGCUGCUACAGUACGUCUUCAGGCUGGAAAUGCUACAGAAGUaCCUGCCAAUUA
 5 ACUGUGCUUUCCUUCUGUGCUUUUGCAGUAGACCCUGCUAAAAGCAUUAaAAGGAUUACCUA
 GCAAGUGGAGGACAACCAAUCACCAACUGUGUGAAGAUGUUGUGUACACACACUGGUACAG
 GACAGGCAAUUACUGUAACACCAGAAGCUAACAUGGACCAAGAGUCCUYUGGUGGUGCUUC
 AUGUUGUCUGUAUUGUAGAUGCCACAUUGACCAUCCAAAUCCUAAAGGAYUCUGUGACUUG
 AAAGGUAAGUACGUCCAAAUACCUACCACUUGUGCUAAUGACCCAGUGGGUUUUACACUUA
 10 GAAACACAGUCUGUACCGUCUGCGGAAUGUGGAAAGGUUAUGGCUGUAGUUGUGACCAACU
 CCGCGAACCUCUAGUCAGUCUGCGGAUGCAUCAMCGUUUUUAAACGGGUUUGCGGUGUAA
 GUGCGACCCGUCUUAACACCGUGCGGCACAGGCACUAGUACUGAUGUCGUCUACAGGGCUUU
 UGAUUAUUACAACGAAAAAGUUGCUGGUUYUGCAAAGUUCCUAAAAACUAA

Translation 1

Nucleotide 3-701 ; 233 aa

LEKMADQAMTQMYKQARSEDKRAKVTSAMQTMFLTMLRKLDNDALNNIINNARDGCVPLNIIPLTAAKLMVV
 VPDYGTYNKTCGNTFTYASALWEIQVVDADSKIVQLSEINMDNSPNLAWPLIVTALRANSVAVKLQNNELSP
 VALRQMSCAAGTTQTACTDDNALAYNNNSKGGRFVLALLSDHQDLKWARFPKSDGTGTIYTELEPPCRFVTD
 20 PKGPKVKYLYFIKA

Translation 2

FKRVCGVSA-ARLTFCGTGTSTDVVYRAFDIYNEKVAGXAKFLK

Alignment 1 of translation 1 sequence

RNA-Dependent RNA Polymerase: bovine coronavirus
 Identities = 181/413 (43%),

Query: 3 LEKMADQAMTQMYKQARSEDKRAKVTSAMQTMFLTMLRKXXXXXXXXXXXXXXXXRDGCVPLN 182
 LE+MAD A+T MYK+AR DK++KV SA+QTMFLF+M+RK GCVPLN
 30 Sbjct: 3985 LERMADLALTNMYKEARINDKRSKVVSALQTMFLFSMVRKLDNQALNSILDNAVKGCVPLN 4044
 Query: 183 IIPLTAAKLMVVVPDYGTYNKTCGNTFTYASALWEIQVVDADSKIVQLSEINMDNSP 362
 IP A L ++VPD Y D TYA +W+IQ + D+D QL+EI+ D +
 35 Sbjct: 4045 AIPSLAANTLTIIVPDKSVYDQVVDNVYVYAGNVWQIQTIQSDGTNKQLNEISDDCN- 4103
 Query: 363 NLAWPLIVTALRAN--SAVKLQNNELSPVALRQMSCAAGTTQTACTDDNALAYNNNSKGG 536
 WPL++ A R N SA LQNNEL P L+ +G QT T YNNNS G
 40 Sbjct: 4104 ---WPLVIIANRHNEVSATVLQNNELMPAKLKTQVNSGPDQTCNTPTQ--CYNNNSNNG 4158
 Query: 537 RFVLALLSDHQDLKWARFPKSDGTGTIYTELEPPCRFVTDTPKGPKVKYLYFIKA*TT*I 716
 + V A+LSD LK+ + K DG + EL+PPC+F KG K+KYLK+K T
 Sbjct: 4159 KIVYAILSDVDGLKYTRILKDDG-NFVVLLEDPCKFTVQDVKGKIKYLYFVKGCNTLA 4217
 45 Query: 717 EVWCWAV*LLQYVFR-----EMLQKYLPIQLCFPSVLLQ*TLKHIKDYLASGGQPI 878
 W V + RL E + LC SV + T L D++ GG PI
 Sbjct: 4218 R--GWVVGTTISSTVRLQAGTATEYASNSSILSLCAFSVDPKKTYL----DFIQGGTPIA 4271
 Query: 879 NCVKMLCTHTGTGQAITVTPEANMDQESXGGASCCLYCRCHIDHPNPKGXCDLKGKVVQI 1058
 NCVKMLC H GTG AITV P+A +Q+S GGAS C+YCR ++HP+ G C L+GK+VQ+
 50 Sbjct: 4272 NCVKMLCDHAGTGMATITVKPDATTNQDSYGGASVCIYCRARVEHPDVGDLCKLRGKRVQV 4331
 Query: 1059 PTTCANDPVGFTRLNRTVCTVCGMWKGYGCSCDQLREPLMQSADASKFLNGFAV 1217
 P DPV + L + VC VCG W+ CSC + +QS D + FLNGF V
 55 Sbjct: 4332 PVG-IKDPVSIVLTHDVCQVCGFWRDGS CSCVS-TDTTVQSKDTN-FLNGFGV 4381

Alignment 2 of translation 2 sequence

RNA-directed RNA polymerase (ORF1B) [murine hepatitis virus]

Identities = 24/44 (54%),

Query: 1199 FKRVCGVSA-ARLTFCGTGTSTDVVYRAFDIYNEKVAGXAKFLK 1327
 FKRV G S ARL PC +G TDV RAFDI N AG + K
 65 Sbjct: 18 FKRVRGTSVNARLVPCASGLDQVQLRAFDICNANRAGIGLYK 61

Fig. 2. Cont.

Note that this sequence is not fully in frame.

5
10

UGACAUCUUACGCGUAUAUGCUAACUUAGGUGAGCGUGUACGCCAAUCAUUAUUAAGACU
GUACAAUUCUGCGAUGCUAUGCGUGAUGCAGGCAUUGUAGGCGUACUGACAUUAGAUAUAUC
AGGAUCUUAUUGGGAACUGGUACGAUUUCGGUGAUUUUCGUACAAGUAGCACCAGGCUGCGG
AGUUCCUAUUGUGGAUUCUAUAUUAUCUAUUGCUGAUGCCCAUCCUCACUUGaCUAGGgCA
UUGGCUGCUGAGUCCcAUAUGGAUGCUGAUCUCGCAAAaCCACUUAUUAaGUGGgAUUUGC
UGAAACAUGAUUUUACGGAAGAGAGACUUUGUCUCUUCGACCGUUAUUUUAAAUAUUGGGA
CCAGACAUAACCAUCCCAAUUGUAUUAACUGUUUGGAUGAUAGGUGUAUCCUUCAUUGUGCA
AaCUUUAAGUGUUAUUUUCUACUGUGUUUcCACCUAACAAGUUUUGGACCACUAGUAAGAA
AAAUUUUGUAGAUGGUGUUCUUCUGUUGUUUCAACUGGAUACCAUUUUCUGAGUAGG
AGUCGUACAUAUUCAGGAUGUAACAUAACAUGCUCGCGUCUCAGUUCAGUUAAGGAACUUUUA
GUGUAUGCUGCUGAUCGAGCUAUGCAUGCAGCUCUUCUGGCAAUUAUUGCUAGAUAAACGCA
CUACAUGCUUUUCAGUAGCUCACUAACAAACAAUGUUGCUUUUCAAACUGUCAAAACCCGG
UAAUUUUAAUAAAGACUUUUAUGACUUUGCUGUGUCUAAA

Translation 1

Nucleotide 2 to 652: Frame 2; 217 aa

20 DILRVYANLGERVQRQSLKTVQFCDMARDAGIVGLVTLTDNQDLNGNWYDFGDFVQVAPGCGVPVIVDSYYSLLM
PILTLTRALAAESHMDADLAKPLIKWDLKHKDFTEERLCLFDYFKYWDQTYHPNCINCLDDRCILHCANFNV
LFSTVFPPTSFGPLVRKIFVDGVPSVSVSTGYHFRELGVVHNQDVNLHSSRLSFKELLVYAADPAMHAASGN

Translation 2

656 to 772: Frame 2; 39 aa

LLDKRTTCFSVAPLTNNVAFQTVKPGNFNKDFYDFAVSK

Alignment

ORF1ab polyprotein Murine hepatitis virus

Identities = 157/257 (61%),

30 Query: 2 DILRVYANLGERVQRSLKTVQFCDAMRDAGIVGLVTLTDNQDLNGNWYDFGDFVQVAPGC 181
DI+ VY LG ++LL T +F DA+ +AG+VGLVTLTDNQDL G WYDFGDFV+ PGC
Sbjct: 4626 DIINVYKKGPIFNRLNTAKFADALVEAGLVGLVTLTDNQDLGYQWYDFGDFVKTVP GC 4685

35 Query: 182 GVPIVDSYSLMLPILTLTRALAAESHMDADLAKPLIKWDLLKHDFTEERLCLEFDYFKY 361
GV + DSYS +MP+LT+ AL +E ++ + +DL+++DFT+ +L LF +YFK+
Sbjct: 4686 GVAVADSYYSYMPMLTMCCHALDSELFVNGTYRE---FDLVQYDFTDFKLELFTKYFKH 4741

40 Query: 362 WDQTYHPNCINCLDDRCILHCANFNVLSTVFPTSFGLPVRKIFVDGVPVSTGYHFR 541
W TYHPN C DDRCI+HCANFN+LFS V P T FGPLVR+IFVDGVP VVS GYH++
sbjct: 4742 WSMTYHPNTCECEDDRCIIHCANFNILFSMVLPKTCFGLVRQIFVDGVPFVVSIGYHYK 4801

Query: 542 ELGVVHNQDVLNLSRSLFKELLVYAADPAMHAASGN+LLDKRTTCFSVAPLTNNVAFQT 721
ELGVV N DV+ H RLS K+LL+YAADPA+H AS + LLD RT CFSVA +T+ V FQT
Sbjct: 4802 ELGVMMNMDVDTHRYRLSLKDLLLYAADPALHVASASALLDLRTCCFSVAAITSGVKFQT 4861

Query: 722 VKPGNFNKFDFYFAVSK 772
VKPGNFN+DFY+F +SK
Sbjct: 4862 VKPGNFNQDFYEFILSK 4878

50 EMC-7 .

50 ACCUUCAGAAUUAUGGUGAAAAUGCUGUUAUACCAMAAAGGAAUAAUGAUGAAUGUCGCAAAGUAUACUCAACU
GUGUCAAUACUUAUAAUACACUUAUAGCUGUACCCUACAACAUGAGAGUUAUUCACUUAUGGUGCUGGCUCU
GAUAAAGGAGUUGCACCAGGUACAGCUGUGCUCAGACAAUGGUUGCCAAUCGGCACACUACUUGUCGAUUCAG
AUCUUAAGUGACUUCGUCUCCGACGCAGAUUCUACUUAUAAUUGGAGACUGUGCAACAGUACAUAACGGCUAAUAA
55 AUGGGACCUUAUUAUAGCGAUUGAUGACCCUAGGACCAACUUGUGACAAAGAGAAUGACUUAAGUAAAGAA
GGGUUUUUCUUAUUCUGUGUGGAUUUAUAAAGCAAAAACUAGCCCUUGGGUGGUUCUAUAGCUGUAAAGAUAA
CAGAGCAUUCUUGGAAUGCUGACCUUUAACAAGCUUAUGGGCCAUUUCUCAUGGUGGACAGCUUUUGUUACAAA
UGUAAAUGCAUCAUCAUCGGAAGCAUUUUAAUUGGGGCUAACUAUCUUGGCAAGCCGAAGGAACAAAUUGAU
GGCUAUACCAUGCUGAUGCUAACUACAUUUCUGGAGGAACACAAUCCUAUCCAGUUGUCUCCUAUUCACUCU
60 UUGACAUAGGACAAAUUCCUUAUAAUUAAGGAGAACUGCUGUAUAGUCUCUUAAGGAGAAUCAAUCAAUGA
UAUGAUUAUUCUCUUCUGGAAAAAGGUAGGCUUAUCAUUAAGAAAACAACAGAGUUGUGGUUUAAGUGAU
AUUCUUGUUAACAACUAAACGAACAUGUUUAUUUCUUAUUUAUUUCUACUCACUAGUGGUAGUGACCUUG
ACCGGUGCACCACUUUUUGAUGAUGUUAAGCUCCUAAUUAACACUCAACAUACUUAUAGAGGGGGGUUA
CUAUCCUGAUGAAAUUUUUAGAUACAGACUCUUAUUUAUACUAGGAUUUAUUUCCAUUUUUAUUCUAAU
65 GUUACAGGGGUUACUACUUAUUAUACUAGCUUUGGCACCCUGUCAUCCUUUAAGGAUGGUUAUUUAUUUG
GUGCCACAGAGAAAACAAUUGUGUCGUGGUUGGGUUUUUGGUUCUACCAUGAACAAAGUCACAGUCGGU

Fig. 2. Cont.

GAUUAUUUAUUAACAAUUCUACUAAUGUUGUUAUACGAGCAUGUAAACUUUGAAUUGUGUGACAACCCUUUCUUU
 GCUGUUUCUAAACCCAUGGGUACACAGACACAUACUAGAUAUUCGAUAAUGCAUUUAAUUGCACUUUCGAGU
 ACAUAUCUGAUGCCUUUUCGCUUGAUGUUUCAGAAAAGUCAGGUAAUUUUAAACACUUACGAGAGUUUGUGUU
 UAAAAUAAAGAUGGGUUUCUCUAUGUUUAUAAAGGGCUAUAACCUUAUAGAUGUAGUUCGUGAUCUACCUUCU
 5 GGUUUUAACACUUUGAAACCUAUUUUUUAAGUUGCCUCUUGGUAUUAACAUUACAAUUUUAGAGCCAUUCUUA
 CAGCCUUUUCACCUGCUCAAGACAUUUGGGGCACGUCAGCUGCAGCCUAUUUUGUUGGCUAUUUAAAGCCAAC
 UACAUUUUAUGCUCAAGUAUGAUGAAAAUGGUACAAUCACAGAUGCUGUUGAUUGUUCUCAAUUCACUUGCU
 GAACUCAAAUGCUCUGUUAAGAGCUUUGAGAUUGACAAAGGAAUUUACCAGACCUCUAAUUUCAGGGUUGUUC
 CCUCAGGAGAUGUUGUGAGAUUCCCUAAUUAUACAAACUUGUGUCCUUUUGGAGAGGUUUUUAAUGCUACUAA
 10 AUUCCCUUCUGUCUAUGCAUGGGAGAGAAAAAAUUUCUAAUUGUGUUGCUAUAUCUCUGUGCUCUACAAC
 UCAACAUUUUUUUAACCUUUUAAGUGCUAUGGCGUUUCUGCCACUAAGUUGAUGAUCUUUGCUUCUCCAAUG
 UCUAUGCAGAUUCUUUUGUAGUCAAGGGAGAUGAUGUAAGACAAUAGCGCCAGGACAAACUGGUGUUAUUGC
 UGAUUUAUAAUUAUAAUUGCCAGAUGAUUUAUGGGUUGUGUCCUUGCUUGGAUACUAGGAACAUUGAUGCU
 ACUUCACACUGGUAUUUAUAAUUAUAAUUAUAGGUUAUCUUGACAUUGGCAAGCUUAGGCCCUUUGAGAGAGACA
 15 UAUCUAAUGUGCCUUUCUCCCGAUGGCAACCUUGCACCCACCUGCUUAAUUGUUAUUGGCCAUUAAA
 UGAUUUAUGGUUUUUAACACCACUACUGGCAUUGGCUACCAACCUUACAGAGUUGUAGUACUUUCUUUUUGAACUU
 UUAUUAUGCACCGGCCACGGUUUGUGGACCAAAUUAUCCAUGACCUUUAUUAAGAACCAGUGUGUCAUUUUUA
 AUUUUAUUGGACUCACUGGUACUGGUGUGUUAACUCCUUCUUAUUAAGAGAUUUAACCAUUUAACAAUUUGG
 CCGUGAUGUUUCUGAUUUCACUGAUUCCGUUCGAGAUCCUAAAACAUUCUGAAUUAUAGACAUUUCACCUUGC
 20 UCUUUUGGGGGUGUAAGUGUAAUUAACACCUUGGAACAAUUGCUUACUUGAAGUUGCUGUUCUAUAUACAAGAUG
 UUAACUGCACUGAUGUUUCUACAGCAAAUUCUACAGCAUACACUACACAGCUGGCGCAUUAUUAUUCUACUGG
 AAACAUGUAUUCAGACUCAAGCAGGCUGUCUUAUAGGAGCUGAGCAUGUCGACACUUCUUAUAGAGUGCGAC
 AUUCCUAUUGGAGCUGGCAUUUGUGCUAGUUACCAUACAGUUUCUUUAUUAACGUAGUACUAGCCAAAAUUCUA
 UUGUGGCUUAUACUAGUCUUUAGGUGCUGAUGUUCUAAUUGCUUACUCUAAUUAACCAUUGCUAUACCUAC
 25 UAACUUUUAUUAUGCAUUAUACAGAAUGUAAUGCCUGUUUCUUAUGGCUAAAACCUCGUGAGAUUGUAUUAUG
 UACAUCUGCGGAGAUUCUACUGAAUGUGCUAAUUGCUUCCCAAUAGGUAGCUUUUGCACACAACUAAUUC
 GUGCACUCUCUGGUUAUUGCUGCUGAACAGGAUCGCAACACAC

Translation 1

30 Nucleotides 3 to 818: Frame 3 272 aa (orf 1ab)
 LQNYGENAVIPQGIMMNVAKYTQLCQYLNTLT LAVPYNMNRVIHFGAGSDKGVAPGTAVLRQWLPTGTLTLLVDSLDNDFVSDA
 DSTLIGDCATVHTANKWDLIISDMYDPRTKHVTENDSKGFFTYLCGFIKQKLALGGSIAVKITEHSWNADLYKLMGHFS
 WWTAFVTNVNASSSEAFLLIGANYLGKPKQIDGYTMHANYIFWRNTNPIQLSSYSLEFDMSEKFLKLRGTAVMSLKENQIND
 35 MIYSLLEKGRLLIRENNRVVSSDILVNN

Translation 2

40 Nucleotide 828 to 3089: Frame 3 756 aa (S protein)
 MFIFLLFLTTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFLFPFYSNVTGFHTINHTFGNPVI
 PFKDIYFAATEKSNVVRGWVFGSTMNNKSQSVIIINNSTNVIRACNFELCDNPFPAVSKPMGTQHTMI FDNFNCTFE
 YISDAFSLDVSEKSGNFKHLREFVFNKNDGFLYVYKGYQPIDVVRDLPSGFNTLKPFIKPLPLGINITNFRAILTAFSPAQD
 IWGTSAAAYFVGYLKPTTFMLKYDENGTTDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPFGDVVRFPNITNLCP
 45 FGEVFNATKFPFSVYAWERKKISNCVADYSVLNSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGGDDVRQIAPGQTGVI
 ADYNYKLDPDDFMGCLAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVFPSPDGKPTPPALNCYWLNDYGEFTT
 TGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFENGLTGTGVLTPSSKRFQPFQFGRDVSDFDTSVRDPKT
 SEILDSPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNNVFQTAGCLIGAHEVDTSYEC
 50 DIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMICYGDS
 ECANLLQYGSFCTQLNRALSWYCC

Alignment 1 of translation 1

55 replicase [bovine coronavirus]
 Identities = 183/271 (67%),

Query: 3 LQNYGENAVIPQGIMMNVAKYTQLCQYLNTLT LAVPYNMNRVIHFGAGSDKGVAPGTAVLR 182
 L NYG+ +P G MMNVAKYTQLCQYLNT TLAVP NMRV+H GAGS+KGVAPG+AVLR
 60 Sbjct: 6822 LWNYGKPVTLPTGCMNNVAKYTQLCQYLNTTTLAVPVNMRVLHLGAGSEKGVAPGSAVLR 6881
 Query: 183 QWLPTGTLTLLVDSLDNDFVSDADSTLIGDCATVHTANKWDLIISDMYDPRTKHVTENDSK 362
 QWLP GT+LVD+DL FVSD+ +T GDC T+ +WDLIISDMYDP TK++ + N SK
 65 Sbjct: 6882 QWLPAGTILVDNDLYPFVSDSVATYFGDCITLFPDCQWDLIISDMYDPITKNIGEYNVSK 6941
 Query: 363 EGFFTYLCGFIKQKLALGGSIAVKITEHSWNADLYKLMGHFSWWTAFVTNVNASSSEAF 542
 +GFFTY+C I+ KLALGGS+A+KITE SWNA+LYKLMG+F++WT F TN NASSSE FL

Fig. 2. Cont.

Sbjct: 6942 DGFFTYICHMIRDKALGGVAIKITEFSWNAELYKLMGYFAFWTVFCTNANASSSEGFL 7001

Query: 543 IGANYLGKPKKEIDGYTMHANYIFWRNTNPIQLSSYSLFDMSEKFLKRGTAVMMSLKENQ 722

5 Sbjct: 7002 IGNYLGKPKVEIDGNVMHANYLFWRNSTVWNGGAYSLFDMSEKFLKLAGTAVINLRADQ 7061

Query: 723 INDMIYSLLEKGRLLIIRENNRVVSSDILVN 815

INDM+YSLLEKG+L++R+ N+ V D LVN

10 Sbjct: 7062 INDMVYSLLEKGRLLVRDTNKEVFGVDSLVD 7092

Alignment 2 (Spike protein of coronavirus)

E2 glycoprotein precursor - murine hepatitis virus (strain JHM); contains spike glycoprotein

15 Identities = 199/798 (24%), Positives = 314/798 (39%), Gaps = 48/798 (6%)
Frame = +3

Query: 828 MFIFLLFLTLTSGSDLDRCCTTFDDVOAPNYTQHTSSM-----RGVYYP-DEI 965
+F+F+L L G D F +Q NY + +S RG YY D +

20 Sbjct: 2 LFVFILLLLPSCGLGYIGD----FRCIQTVNNGNNASAPSISTEAVDVSKGRGTYVLDVRV 57

Query: 966 FRSDTLTYLTQDLFLPF----YSNV--TGFTHTINHTFGNP--VIPFKDGIYFAATE-KSNV 1118
+ + TL LT + P Y N+ TG +T++ T+ P + F DGI+ K+N

25 Sbjct: 58 YLNATLLLTG--YYPVDGNSYRNLALTGTNTLSLTWFKPPFLSEFNDGIFAKVQNLKTNT 115

Query: 1119 VRGW-----VFGSTMNNKXXXXXXXXXXXXXXXXXACNFECDNPFPAVSKPMGTQHT 1277
G V GS N C + +C P+ KP

Sbjct: 116 PTGATSYFPTIVIGSLFGNTSYTVVLEPYNNIIMASVCTYTICQLPY-TPCKP----- 167

30 Query: 1278 MIFDNAFNCTFEYISDAFSLDVSEKSGNEFKHLREFVFKNKDGFYLYVY---KGYQPIDVVR 1448

N + + DV K R F F +LY + +G

Sbjct: 168 -----NTNGNRVIGFWHTDVKKPICLLK--RNFTFNVNAPWLYFHFYQQGGTFYAYYA 218

35 Query: 1449 DLPSGFNTLKPIFKPLGINITNFRAILTAFSPAQDIWGTSAAYFVGYLKPTTEMLKYD 1628
D PS L F + +G +T + + +P T A Y+V L ++ ++

Sbjct: 219 DKPSATTFL---FSVYIGDILTQYFVLPPFICTPTAG--STLAPLYWVTPLLKRQYLFNFN 273

Query: 1629 ENGTITDAVDCSQNPLAELKCSVKSEIDKGIYQTSNFRVPSGDVVR-FPNITNLCFPG 1805
E G IT AVDC+ + +E+KC +S G+Y S + V P G V R PN+ + C

40 Sbjct: 274 EKGVITSAVDCASSYISEIKCKTQSLPSTGVYDLSGYTVQPVGVVYRRVNPPLD-CKIE 332

Query: 1806 EVFNATKFPSVYAWERKKISNCVADYSLYNSTFFSTFKCYGVSATKLNLCFSNVYADS 1985
E A PS WER+ NC + S L + C + A+K+ +CF +V D

45 Sbjct: 333 EWLTAKSVPSPNLWERRTFQNCNENLSSLLRYVQAESLSCNNIDASKVYGMCFGSVSVDK 392

Query: 1986 FVVKGDVVRQIAPGQTGVADYNYKLPPDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHG 2165
F + + G +G + NYK+ C L ++ + T NYN R+G

Sbjct: 393 FAIPRSRQIDLQIGNSGFLQTANYKIDTAATSCQLYYSLPKNNVT-INNNPSSWNRARYG 451

50 Query: 2166 KLRPFERDISNVFSPDGKPCPTPALNCYWPLNDYGFYTTTGIGYQPYRVVLSFELLNA 2345

+ +ND R + + LLN

Sbjct: 452 -----FKVND-----RCQIFANILLNG 468

55 Query: 2346 --PATVCGPKL---STDLIKQCVNFNFGLTGTGVLTLP-SSKRFQPFQFGRDVSDFTD 2507
T C L +T++ CV ++ G+TG GV + + +Q DV+ +

Sbjct: 469 INSGTTCSTDLQLPNTTEVATGVCVRYDLYGITGQGVFKEVKADYNSWQALLYDVNGNLN 528

Query: 2508 SVRDPKTSEILDISPCSEFGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWR 2687
RD T++ I C G VS + E A+LY+++NC+ V T + + P

60 Sbjct: 529 GFRDLTNTKTYTIRSCYSGRVSAAY--HKEAPEPALLYRNINCSYVFTNNISREENPL-- 584

Query: 2688 IYSTGNNVFQTOAGCLIGAEH--VDTSYECDIPIGAGICASYHTVSLLR---STSQK--S 2846
N F + GC++ A++ + C++ +GAG+C Y R ST + +

65 Sbjct: 585 -----NYFDSYLGCVVNADNRTDEALPNCNLRMGAGLCVDYSKRRARRSVSTGYRLTT 638

Query: 2847 IVAYTMSLGADSSIAYSN-NTIAIPTNFSISITTEVMPVSMKTSVDCNMICYGDSTECA 3023
Y L DS + + IPTNF+I E + + K ++DC ++CGD+ C

Sbjct: 639 FEPYMPMLVNDVSVQSVGGYEMQIPTNFTIGHHEEFIQIRAPKVTIDCAAFVCGDNAACR 698

70 Query: 3024 NLLLQYGSFCTQLNRALS 3077

Fig. 2. Cont.

L++YGSFC +N L+
 Sbjct: 699 QQLVEYGSFCDNVNAILN 716

RDG1 seq

5 UUCAAGGCcUCAAACNUAUGUAAACACAACAACUAAUCAGGGMUGcUGAAAUCHCGSCUUCUGCUAAUCUUGC
 UGCUACUAAAAUGUCUGAGUGUGUUCUUGGACAAUCAAAGAGUUGACUUUUGUGGAAAGGGCUACCACCUU
 AUGUCCUCCCACAAGCAGCCCCGCAUGGUGUUGUCUCCUACAUGUCACGUAUGUGCCAUCCCAGGAGAGGA
 10 ACUUCACCACAGCGCCAGCAAUUUGUCAUGAAGGCAAAGCAUACUCCUCGUGAAGGUGUUUUUGUGUUUAA
 UGGCACUUCUUGGUUUUAUUACACAGAGGAACUUCUUUUCUCCACAAAUAUUACUACAGACAAUACAUUGUC
 UCAGGAAAUUGUGAUGUCGUUAUUGGCAUCAUUAACAACACAGUUUAUGAUCCUCUGCAACCUGAGCUUGACU
 CAUUCAAAGAAGAGCUGGACAAGUACUCAAUUAUACAUCACCAGAUGUUGAUCUUGGCGACAUUUCAGG
 CAUUAACGCUUCUGUCGUAACAUAUCAAAGAAAUUGACCGCCUCAUGAGGUGCGUAAAAUUUAAUGAA
 UCACUCAUUGACCUCAAGAAUUGGGAAAAUAUGAGCAAUAUAUUAAGUGgCCCUGGUACGUCUGGGU

Translation 1

Nucleotides 3 to 650: Frame 3; 216 aa

QSLQXYVTQQLIRXAEIXXSANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAIC
 20 HEGKAYFPREGVVFENGTSWFITQRNFFSPQIITTDNTFVSGNCDVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPD
 VDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVW

Translation 2

Nucleotides 37 to 339: Frame 1; 101 aa

SGXLKXXLLILLKLSVFLDNQKELTFVERATTLCPSHKQPRMVLSYSMRMCHPRRGTSPPQRQQFVMKAKHTSLVKV
 25 FLCMLALLGLLHRGTSFLHK

Translation 3

Nucleotides 343 to 576: Frame 1; 78 aa

LLQTIHLSQEIIVMSLLASLTTFMILCNLSLTHSKSWTSTSKIHHQMLLILATFQALTLLSSTFKKLTASMRSLKI
 30

Alignment of translation 1

S glycoprotein [murine hepatitis virus]
 Length = 1376

35 Identities = 86/218 (39%), Positives = 129/218 (59%), Gaps = 3/218 (1%)
 Frame = +3

Query: 6 SLQTYVTQQLIRXAEIXXSANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVF 185
 +L Y+++QL I SA A K++ECV Q+ R++FCG G H++S Q AP+G+ F
 40 Sbjct: 1105 ALNAYISKQLSDSTLIKFSAAQAIEKVNCEVKSQTTRINFCGNGNHILSLVQNAPYGLYF 1164

Query: 186 LHVITYVPSQERNFTTAPAICHEG-KAYFPREGVVFENGTSWFITQRNFFSPQIITTDNTF 362
 +H +YVP+ +P +C G + P+ G FV + W T +++ P+ IT N+
 45 Sbjct: 1165 IHFSYVPTSFTTANVSPGLCISGDRGLAPKAGYFVQDDGEWKFSGSSYYYPEPITDKNSV 1224

Query: 363 VSGNCDVIGIINNTVYDPLQPELDSFKEELDKYFKNHTS--PDVDLGDISGINASVVNI 536
 V +C V +P + L FKEELDK+FKN TS PD+ L D +N + +++
 Sbjct: 1225 VMSSCSVNYTKAPEVLLNSSIPNLPDFKEELDKWFKNQTSIAPDLSL-DFEKLNVTFDL 1283

50 Query: 537 QKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVW 650
 E++R+ E K LNES I+L+E+G YE Y+KWPWYVW
 Sbjct: 1284 SDEMNRIQEAIKKLNESYINLKEVGTYEMYVKWPWYVW 1321

EMC-8

AGGCCAAAACAGCGCCGACCCCAAGGUUUACCCAAUAAUACUGCGUCUUGGUUCACAGCUCUCACUCAGCAUG
 GCAAGGAGGAACUUAGAUAUCCUCGAGGCCAGGGCGUCCAUAACACCAAUAGUGGUCCAGAUGACCAAAU
 UGGCUACUACCGAAGAGCUACCCGACGAGUUCGUGGUGGUGACGGCAAAAUGAAAGAGCUCAGCCCCAGAUGG
 60 UACUUCUAUUACCUAGGAACUGGCCCCAGAAGCUUCACUCCCUACGGCGCUAACAAGAAGGCAUCGUUAGGG
 UUGCAACUGAGGGAGCCUUGAAUACACCCAAAGACCACAUUGGCACCCGCAAUCCUAAUAAUAAUGUUGCC

Translation

Nucleotides 1 to 363: Frame 1; 121 aa

RPKQRRPQGLPNNTASWFTALTQHGKEELRFRGQGVPIINTNSGPDQIGYRRATRRVRGGDGKMKELSPRWYFYLLGTG
 65 PEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNXA

Fig. 2. Cont.

Alignment

nucleocapsid protein - bovine coronavirus (strain Mebus)

5 Identities = 55/129 (42%),

Query: 1 RPKORRPOGLPNNTA-----SWFTALTQHGK-EELRFPRGQGVPIINTNSGPDQIGYYRR 162

+PKQ LP+ SWF+ +TQ K +E F GQGVPI + GY+ R

10 Sbjct: 44 QPKQTATSQLPSGGNVVPYYSWFSGITQFQKGKEFEFAEGQGVPIAPGVPATEARGYWYR 103

Query: 163 ATRR-VRGGDGKMKELSPRWYFYLLGTGPEASLPYGANKEGIVVWATEGA-LNTPKDHIG 336

RR + DG ++L PRWYFYLLGTGP A YG + +G+ WVA+ A +NTP D I

Sbjct: 104 HNRRSFKTADGNQRQLLPRWYFYLLGTGPHAKDQYGTIDGVFVWASNQADVNTPAD-IL 162

15 Query: 337 TRNPNNNXA 363

R+P+++ A

Sbjct: 163 DRDPSSDEA 171

EMC-11: unknown sequence

20 UUGCAUACCGCAAUGUUCUUCUUCGUAAGAACGGUaAUAAGGGAGCCGGUGGUCUAUAGCUgUGGCAUGAUCUA
 AAGUCUUAUGACUUAAGGUGACGAGCUUUGGCACUGAUCCCAUUGAAGAUUAUGAACAAAACUGGAACACUAAGC
 AUGGCAGUGGGUGACUCUCCGUGAACUCACUCGUGAGCUCUAUGGAGGUGCAGUCACUCGCUAUGUCGACAACAA
 UUCUGUGGGCCAGAUUGGUACCCUCUUGAUUGCAUCAAGAUUUUCUCGCACGCGCGGGCAAGUCAUGUGC
 25 ACUCUUCCGAACAACUUGAUUACAUCGAGUCGaAGAGAGGUGUCUACUGCUGCCGUGACCAUGAGCAUGAAA
 UUGCCUgGGUUCACUGAGCGCUCUGAUAAAGAGCUACGAGCACCAGACACCCUUCGaAAUUAAGAGUGCCAAGA
 AAaUUGACACUUAUCAAAGGGGAAUGCCCCAAAGCUUGUGUUUCCUCUUAACUCAAAGUCAAGUCAUUCAA
 CCACGUGUUGAAAAGAAAAAGACUGAGGGUUUCAUGGGGCGUAUACGCUCUGUGUACCCUGUUGCAUUCACC
 AGGAGUGUAACAAUAGCACUUGUCUACCUUGAUGAAUGUAUUAUUGCGAUGAAGCUUCAUGGCAGACGUG
 CGACUUUCUGAAAGCCACUUGUGAACAUUGUGGCACUGAAAUUUAGUUAUUGAAGGACCUAGUACAUGUGGG
 30 UACCUACCUACUAAUGCUGUAGUGAAAAUGCCAUGUCCUGCCUGUCAAGACCCAGAGAUUGGACCUAGCAUA
 GUGUUGCAGAUUAUCACAACCACUCAAAAUUGAAACUCGACUCCGCAAGGGAGGUAGGACUAGAUGUUUUGG
 AGGUGUGUGUUUGCCUAUGUUGGUGCUAUAUAAGCGUGCCUACUGGGUUCUUGUGCUAGUGCUGAUUU
 GGCUCAGGCCAUACUGGCAUUAUGUGGAGACCAUGUGGAGACCUUGAAUGAGGAUUCUUGAGAUACUGAGUC
 GUGAACGUGUUAACAUUAACAUUGUUGGCGAUUUUCAUUUGAUGAAGAGGUUGCCAUCAYUUUGGCAUCYUU
 35 CUCUGCUUCUACAAGUGCCUUUAUUGACACUAUAAGAGAGUCUUGAUAACAAGUCUUUCAAACCAUUGUUGAG
 UCCUGCGGUAACUAUAAGUUACCAAGGGAAAGCCCGUAAAAGGUGUCUUGGAACAUGGACAACAGAGAUACAG
 UUUUAACACCACUGUGUGGUUUUCCUCACAGGCUGCUGGUGUUAUCAGAUCAAUUUUUGCGCGCACACUUGA
 UGCAGCAAACCACUCAAUUCCUGAUUUUGCAAAGAGCAGCUGUCACCAUACUUGAUGGUUAUUUCUGAACAGUCA
 UUACGUCUUGUCGACGCCAUGGUUUUAUACUUCAGACCUGCUCACCAACAGUGUCAUUAUUAUGGCAUAUGUAA
 40 CUGGUGGUCUUGUACAACAGACU

Translation of putative open reading frames

45 >~out: 78 to 1: Frame -2 26 aa
 DFRSCHSYDHRLPYRSYEEHCGMQ
 >~out: 59 to 379: Frame 2 107 aa
 LWHDLKSYDLGDELGTDPIDYEQNWNTHKSGALRELTRELNNGAVTRYVDNNFCGPDGYPLDCIKDFLARAGKSMCTLS
 EQLDYIESKRGVYCCRDHEHEIAWVH
 50 >~out: 283 to 89: Frame -1 65 aa
 LARACEKIFDAIKRVPWATEIVVDIASDCTSIELTSEFTECTAMLSVPVLFIIIFNGISAKLVT
 >~out: 90 to 614: Frame 3 175 aa
 VTSALALIPLKIMNKTGLSMVAVHSVNSLVSSMEVQSLAMSTTISVAQMGTLIIASKIFSHARASQCALFPNNLITSSRRE
 VSTAAVTMSMKLPGFTERS DKSIEHQTPFEIKSAKKIDTFKRGMPQSLCFLLTQKS KSFNHVLKRRLRVSWGVYALCTLL
 55 HLHRSVTICTLP
 >~out: 204 to 124: Frame -2 27 aa
 RVTAPPLSSRVSSRSAPLPCLVFQFCS
 >~out: 312 to 208: Frame -2 35 aa
 SSCSERVHIDLPARARKSLMQSRGYPSGPQKLLST
 60 >~out: 485 to 258: Frame -3 76 aa
 EETQALGHSPFESVNFGLTNFEGCLVLVALIRALSEPRQFHAHGHGSSRHLSSTRCNQVVRKECTLTCPRVREN
 >~out: 397 to 287: Frame -1 37 aa
 LLSERSVNPNGFMLMVTAAVDTSRLDVIKLFKSAH
 >~out: 364 to 486: Frame 1 41 aa
 65 NCLGSLALIRATSTRHPSKLRVPRKLTLSKGECPKACVSS
 >~out: 490 to 401: Frame -1 30 aa
 VKRKHLWGIPLLVKVSIFLALLISKGVWCS
 >~out: 446 to 1483: Frame 2 346 aa

EMC12: unknown sequence .

Translation of putative open reading frames

```

>~out: 3 to 446: Frame 3          148 aa
LAHAETTRKLMPICMVDVRAIMATIQRKYKGIKIQEGIVDYGVRRFFFTYSKEPVASIITKLNSLNEPLVTMPIGYVTHGFNL
55 EEAARCMRSLKAPAVSVSSPDAVTTYNGYLTSSSKTSEEHFVETVSLAGSYRDWSYSGQRTTELGV
>~out: 100 to 11: Frame -2        30 aa
ILIPLYLRWMVAIMALTSMHIGINFLVSSA
>~out: 188 to 33: Frame -1        52 aa
RVQLRNNRSYRLFTSIKEESDTIVNDALLNFNSFILTLDGCHYGSNIHAYRH
60 >~out: 64 to 159: Frame 1        32 aa
WQPSNVSIKELKFKRASLTMVSDSSFILVKSL
>~out: 220 to 143: Frame -2       26 aa
PIGIVTSGSFRFESFVIEATGSLLV
>~out: 293 to 192: Frame -1       34 aa
65 HYGRSFKRTHHTARSLFKIKTMCHITNWHCDKRLI
>~out: 397 to 224: Frame -2       58 aa
EPAKETVSTKCSSDVFDEVRYPYVVTASGDDTDTTAGALRERIQRASSRLKPCVT
>~out: 229 to 288: Frame 1        20 aa

```

Fig. 2. Cont.

```

      HMVLILKRLRAVCVLLKLLP
      >~out: 292 to 372: Frame 1      27 aa
      CQYHHQMLLLHIMDTSLRHQRHLRSTL
      >~out: 444 to 340: Frame -3     35 aa
5     QHLTLYAVLNRTNLCKSQPKKLFQSAPQMSLMTK
      >~out: 416 to 351: Frame -1     22 aa
      IGPISVRASQRNCFYKVLLRCL
      >~out: 365 to 445: Frame 2      27 aa
      GALCRNSFFGWLLQRLVLFRTAYRVRC
10    >~out: 376 to 435: Frame 1     20 aa
      KQFLWLALTEIGPIQDSVQS
```

15

Figure 3.

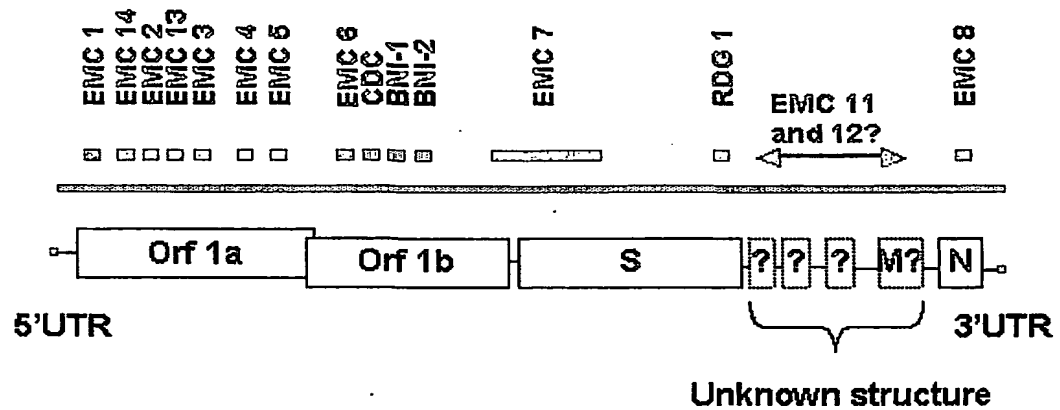


Figure 4.

Comparison of N-termini of the S proteins of the group 2 coronaviruses

5

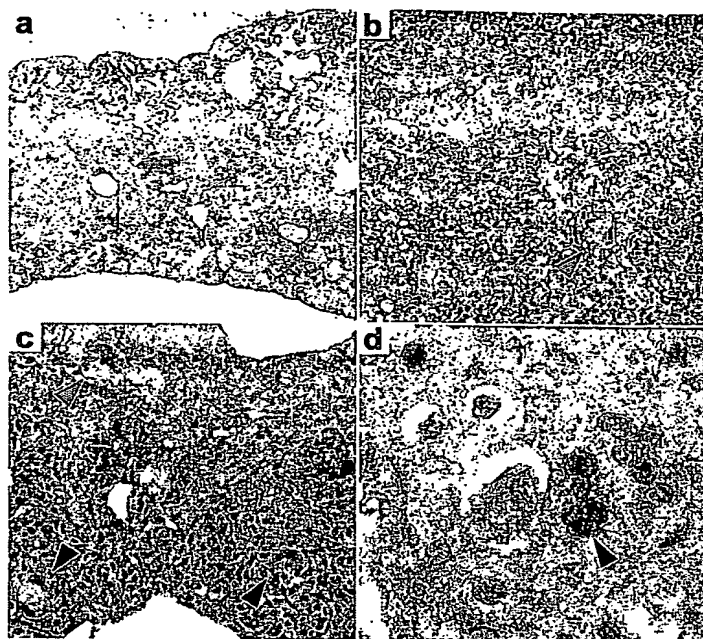
HCV OC43	MFLILLISLPTAFAVIGDL- KCTTVS INDID
MHV A59	MLFVFILFLPSCLGIGDF- RCIQLVNS NGA
BCV	MFLILLISLPMFAVIGDL- KCTTVS INDVD
SARS	MF-IFLLEFL-TLTSG-SDLDRCTTFDDVQAP

10

Figure 5.



Figure 6.



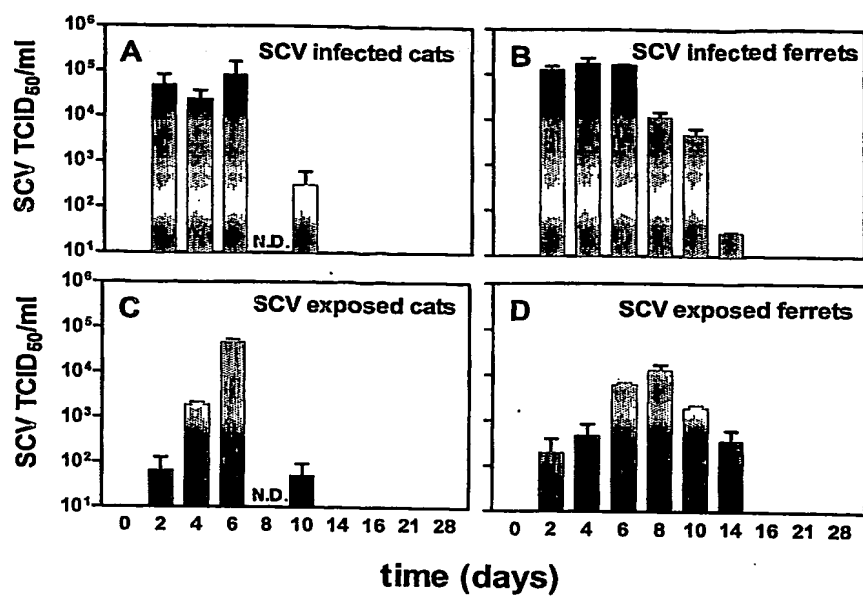


Figure 7.

Figure 8 Detection of SCV in postmortem tissues of experimentally SCV infected cats and ferrets

Tissue	Cats				Ferrets			
	1	2	3	4	1	2	3 [†]	4
Trachea	+/	+/	+/	+/	+/	+/	+/	+/
Lung	+*	+	+	+	+	+	+	+
Tracheo-bronchial lymph node	+/	+/	+/	+/	+/	+/	+/	+/
Duodenum	-/-	-/-	-/-	-/-	-/-	-/-	-/-	-/-
Jejunum	-/-	-/-	-/-	-/-	-/-	-/-	-/-	-/-
Ileum	-/-	-/-	-/-	-/-	-/-	-/-	-/-	-/-
Mesenteric lymph node	-/-	-/-	-/-	-/-	-/-	-/-	-/-	-/-
Kidney	-/-	-/-	-/-	-/-	-/-	-/-	-/-	-/-
Urinary bladder	-/-	-/-	-/-	-/-	-/-	-/-	-/-	-/-
Peripheral blood mononuclear cells	-/-	-/-	-/-	-/-	-/-	-/-	-/-	-/-

* virus isolation/real time PCR results are depicted at day 4 p.i.

[†] died during the experiment.

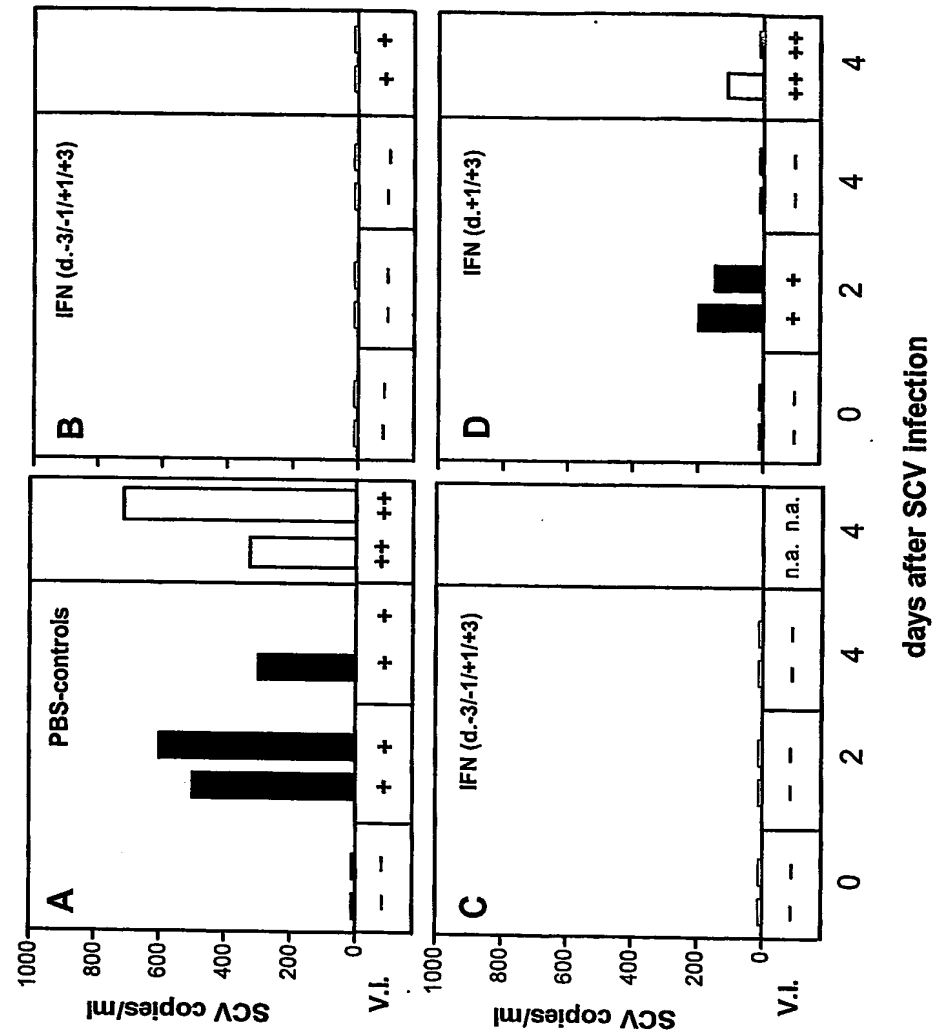


Figure 9

Figure 10

1 atattaggtt tttaacctacc caggaaaagc caaccaacct cgatctcttg tagatctgtt
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 121 gcagtataaa caataataaa ttttactgtc gttgacaaga aacgagtaac tcgtccctct
 181 tctgcagact gcttaacggtt tgcgtcgtgt tgcagtcgat catcagcata cctagggttc
 241 gtccgggtgt gaccgaaagg taagatggag agccttggtc ttggtgtcaa cgagaaaaaa
 301 cactgtccaa tcagtgttgc tgccttccag gttagagacg tgcataccta cacttggtg
 361 gactctgtgg aagaggccct atcggaggca cgtgaacacc tcaaaaatgg cacttggtg
 421 ctatgtagc tggaaaagg cgtactgcc cagcttgac agcctatgt gttcattaaa
 481 cgttctgag ccttaagcac caatcagcgc cacaaggtcg ttgagctggt tgcagaaatg
 541 gacggcattc agtacggctg tagcggata acactgggag tactcgtgcc acatgtgggc
 601 gaaaccccaa ttgcataccg caatgttctt cttcgttaaga acgttaataa gggagccggt
 661 ggtcatagct atggcatcga tctaaagtct tatgacttag gtgacgagct tggcactgat
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 781 ctactcgtg agtcaaatgg aggtgcagtc actcgtatg tgcacaaca tttctgtggc
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 961 gaccatgagc atgaaattgc ctggttcaat gagcgtctg ataagagcta cgagcaccag
 1021 acacccttcg aaattaagag tgccaagaaa ttgacacct tcaaaaggga atgcccacaa
 1081 ttgtgtgttc ctcttaactc aagtgtaaaa gtcattcaac cactgttga aaagaaaaag
 1141 actgaggggt tcatggggcg tatacgtctt gtgtaccctt ttgcatctcc acaggagtgt
 1201 aacaatatgc acttgtctac cttgtgaaa tgtaatcatt gcgatgaagt ttcattggag
 1261 acgtgcgact ttctgaaagc cacttgtgaa cattgtggca ctgaaaaattt agttattgaa
 1321 ggacctacta catgtgggta cctacactat aatgctgtag tgaaaatgcc atgtcctgcc
 1381 tgtcaagacc cagagattgg acctgagcat agtgttgag attatcaca cactcaaac
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 1801 aagggaagc ccgtaaaaag tgccttgaac atttgacaac agagatcagt tttacacca
 1861 ctgtgtgggt ttccctcaca ggtgtggtgt gttatcagat caatttttgc gcacacactt
 1921 gatgeagcaa accactcaat tctgtatttg caaagagcag ctgtcaccat actgatggtt
 1981 atttctgaac agtcattacg tcttgcagac gccatgggtt atacttcaga cctgctcacc
 2041 aacagtgtca ttattatggc atatgtaact ggtgtgtctg tacaacagac ttctcagtgg
 2101 ttgtctaatac ttttgggcac tactgttgaa aaactcaggc ctatctttga atggattgag
 2161 gcgaaactta gtgcaggagt tgaatttctc aaggatgctt gggagattct caaatttctc

Fig. 10. Cont

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 2281 gattgtgtaa aatgcttcat tgatgttgtt aacaaggcac tcgaaatgtg cattgatcaa
 2341 gcaactatcg ctggcgcaaa gttgcgatca ctcaacttag gtgaagtctt catcgctcaa
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 2461 cttaaaggac caaagaagt aacctttctt gaagtgtatt cacatgacac agtacttacc
 2521 tctgaggagg ttgtttctaa gaacggtgaa ctgaaagcac tcgagacgcc cgttgatagc
 2581 ttcacaaatg gagctatcgt tggcacacca gtctgtgtaa atggcctcat gctcttagag
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 2941 aacatgggta acttttcac acgtatgtat gttcctttt accctccaga tgatgatgct
 3001 ggtgaagaaa acttttcac acgtatgtat gttcctttt accctccaga tgatgatgct
 3061 gaggcagatg cagagtgtga ggaagaagaa attgatgaaa cctgtgaaca tgagtaacgg
 3121 acagaggatg attatcaagg tctcctctcg gaatttggtg cctcagctga aacagttcga
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 3241 ccagaccag aacctacac tgaagaacca gttaatcagt ttactgggtt tttaaaactt
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 3361 atgtgtgattg taaatgctgc taacatacac ctgaacacatg gtggtggtg agcaggtgca
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 4561 tttaatcttg aagaggctgc gcgctgtatg cgttctctta aagctcctgc cgtagtgtca
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30

35

40

Fig. 10. Cont.

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Fig. 10. Cont.

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Fig. 10. Cont.

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Fig 10. Cont.

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Fig 10. Cont.

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Fig. 10. Cont.

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Fig. 10. Cont.

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Fig. 10. Cont.

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Fig. 10. Cont.

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Fig. 10. Cont.

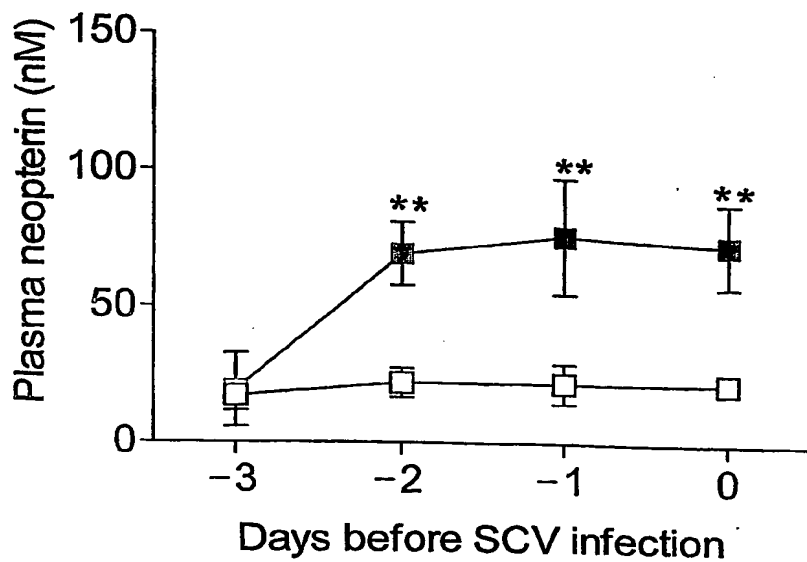
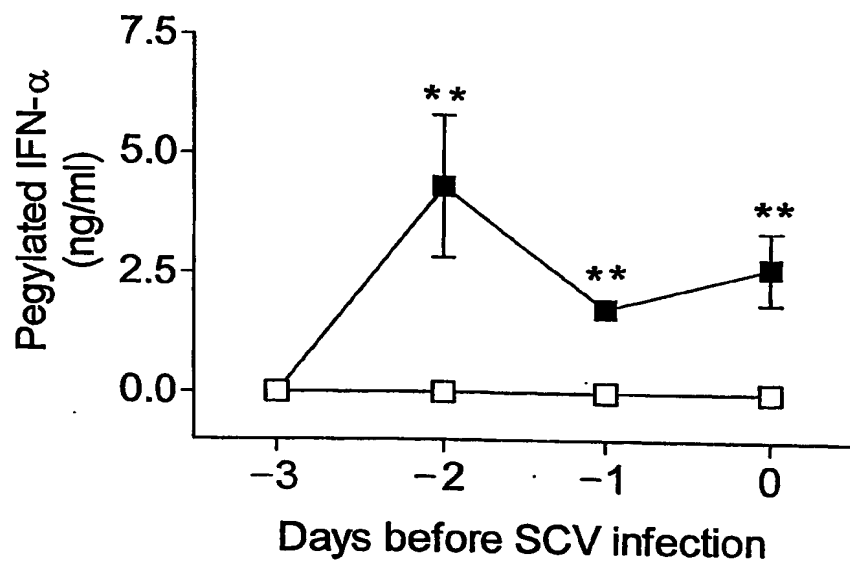
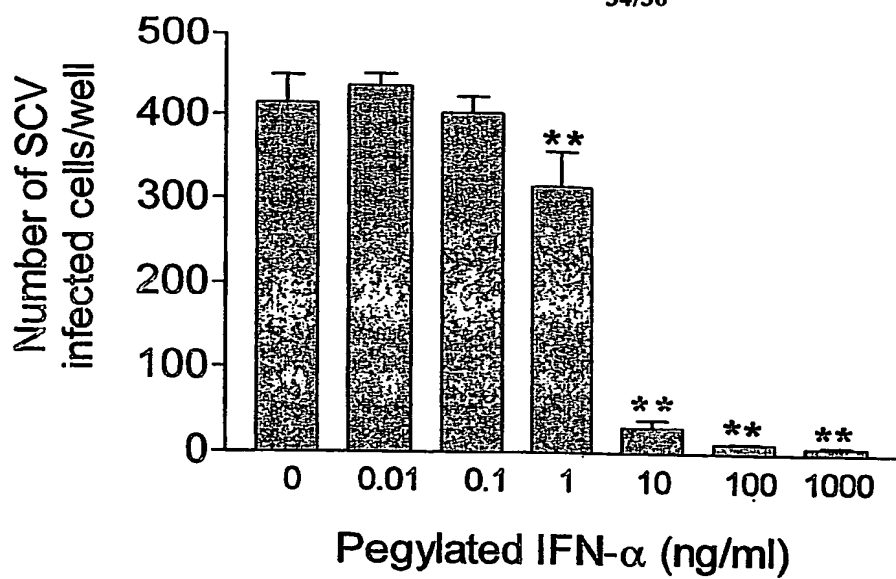
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Fig. 10. Cont.

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Fig 11



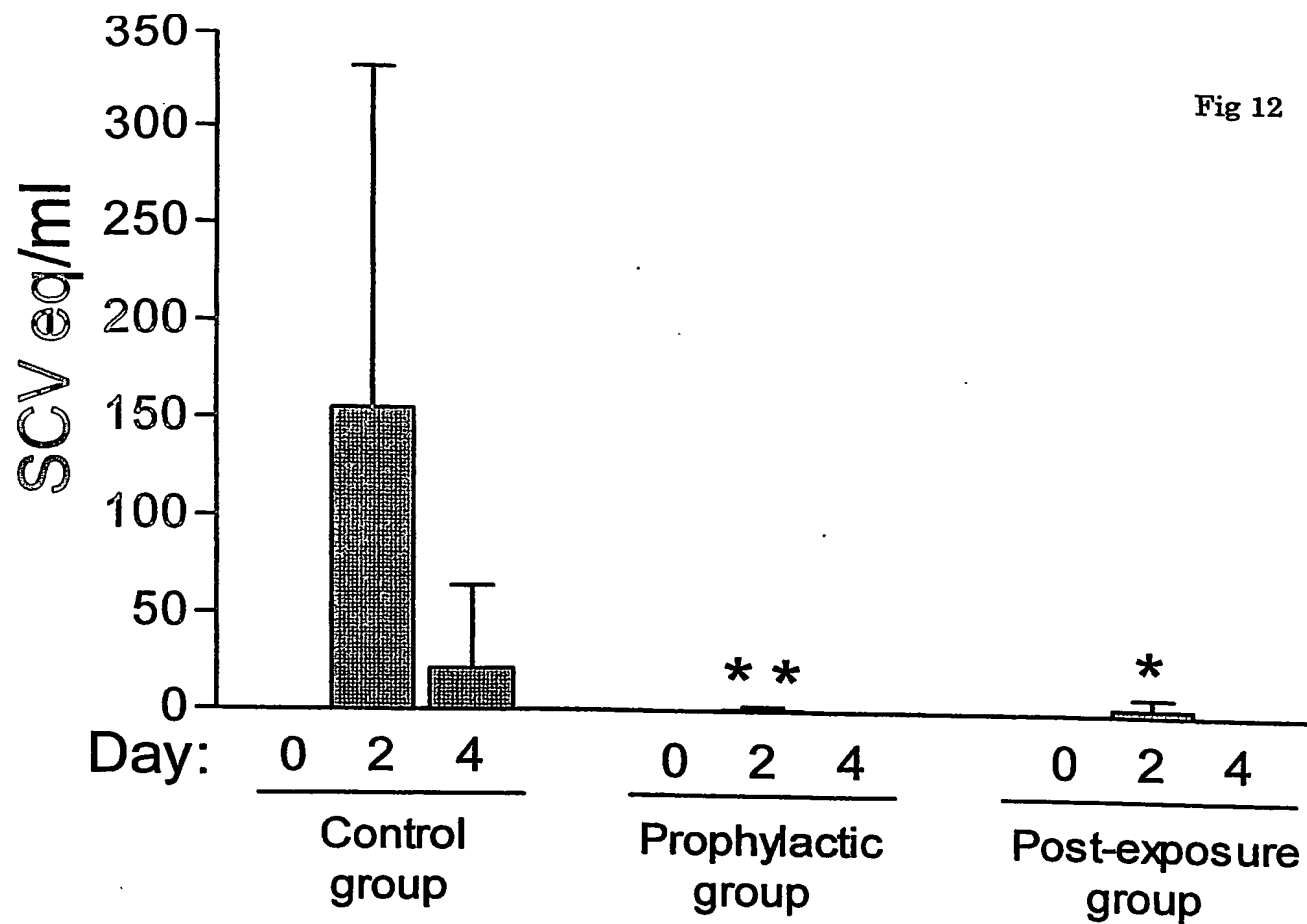


Fig 13

